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TECH CENTER 1600/2900

RAW SEQUENCE LISTING   DATE: 05/04/2001
PATENT APPLICATION: US/09/842,347   TIME: 12:40:33

Input Set : N:\Crf3\RULE60\09842347.txt
Output Set: N:\CRF3\05042001\I842347.raw

SEQUENCE LISTING

```
 4·(1) GENERAL INFORMATION:
 6       (i) APPLICANT: TAKAHASHI, Tohru
 7                      SERIZAWA, Nobufusa
 8                      KOISHI, Ryuta
 9                      KAWASHIMA, Ichiro
11      (ii) TITLE OF INVENTION: EXPRESSION SYSTEMS UTILIZING
12                               AUTOLYZING FUSION PROTEINS
13                               AND A NOVEL REDUCING POLYPEPTIDE
15     (iii) NUMBER OF SEQUENCES: 19
17      (iv) CORRESPONDENCE ADDRESS:
18           (A) ADDRESSEE: Frishhauf, Holtz, Goodman, Langer & Chick, P.C.
19           (B) STREET: 767 Third Avenue-25th Floor
20           (C) CITY: New York
21           (D) STATE: New York
22           (E) COUNTRY: United States
23           (F) ZIP: 10017-2023
25       (v) COMPUTER READABLE FORM:
26           (A) MEDIUM TYPE: Floppy disk
27           (B) COMPUTER: IBM PC compatible
28           (C) OPERATING SYSTEM: PC-DOS/MS-DOS
29           (D) SOFTWARE: PatentIn Release #1.24
31      (vi) CURRENT APPLICATION DATA:
C-->32       (A) APPLICATION NUMBER: US/09/842,347
C-->33       (B) FILING DATE: 25-Apr-2001
34           (C) CLASSIFICATION:
44     (vii) PRIOR APPLICATION DATA:
37           (A) APPLICATION NUMBER: 09/167,151
38           (B) FILING DATE:
41           (A) APPLICATION NUMBER: JP 6-218392
42           (B) FILING DATE: 13-SEP-1994
45           (A) APPLICATION NUMBER: JP 6-303809
46           (B) FILING DATE: 07-DEC-1994
48    (viii) ATTORNEY/AGENT INFORMATION:
49           (A) NAME: Goodman, Herbert
50           (B) REGISTRATION NUMBER: 17081
51           (C) REFERENCE/DOCKET NUMBER: 950376/HG
53      (ix) TELECOMMUNICATION INFORMATION:
54           (A) TELEPHONE: (212) 319-4900
55           (B) TELEFAX: (212) 319-5101
56           (C) TELEX: 236268
59 (2) INFORMATION FOR SEQ ID NO: 1:
61       (i) SEQUENCE CHARACTERISTICS:
62           (A) LENGTH: 1320 base pairs
63           (B) TYPE: nucleic acid
64           (C) STRANDEDNESS: double
65           (D) TOPOLOGY: linear
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        67      (ii) MOLECULE TYPE: cDNA to mRNA
W--> 69      (iii) HYPOTHETICAL: N
W--> 71      (iv) ANTI-SENSE: N
        73      (vi) ORIGINAL SOURCE:
        74          (A) ORGANISM: Clover Yellow Vein Virus
        76      (ix) FEATURE:
        77          (A) NAME/KEY: CDS
        78          (B) LOCATION: 1..1320
        79          (D) OTHER INFORMATION:
        80      (ix) FEATURE:
        81          (A) NAME/KEY: mat_peptide
        82          (B) LOCATION: 10..1311
        83          (D) OTHER INFORMATION:
        87      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
        89 AAG TTC CAA GGG AAA AGT AAG AGA ACA AGA CAA AAG TTG AAG TTC AGA      48
        90 Lys Phe Gln Gly Lys Ser Lys Arg Thr Arg Gln Lys Leu Lys Phe Arg
        91  1           5               10               15
        93 GCG GCA AGA GAC ATG AAG GAT CGT TAT GAA GTG CAT GCC GAT GAG GGG      96
        94 Ala Ala Arg Asp Met Lys Asp Arg Tyr Glu Val His Ala Asp Glu Gly
        95           20              25              30
        97 ACT TTA GTG GAA AAT TTT GGA ACT CGT TAT TCA AAG AAA GGC AAG ACA      144
        98 Thr Leu Val Glu Asn Phe Gly Thr Arg Tyr Ser Lys Lys Gly Lys Thr
        99           35              40              45
       101 AAA GGT ACT GTT GTG GGT TTG GGT GCA AAA ACA AGA CGG TTC ACT AAC      192
       102 Lys Gly Thr Val Val Gly Leu Gly Ala Lys Thr Arg Arg Phe Thr Asn
       103           50              55              60
       105 ATG TAT GGT TTT GAC CCC ACG GAG TAT TCA TTT GCT AGG TAT CTT GAT      240
       106 Met Tyr Gly Phe Asp Pro Thr Glu Tyr Ser Phe Ala Arg Tyr Leu Asp
       107  65              70              75              80
       109 CCA ATC ACG GGT GCA ACA TTG GAT GAA ACC CCA ATT CAC AAT GTA AAT      288
       110 Pro Ile Thr Gly Ala Thr Leu Asp Glu Thr Pro Ile His Asn Val Asn
       111           85              90              95
       113 TTG GTT GCT GAG CAT TTT GGC GAC ATA AGG CTT GAT ATG GTT GAC AAG      336
       114 Leu Val Ala Glu His Phe Gly Asp Ile Arg Leu Asp Met Val Asp Lys
W--> 115           100             105             110
       117 GAG TTA CTT GAC AAA CAG CAC TTA TAC CTC AAG AGA CCA ATA GAA TGT      384
       118 Glu Leu Leu Asp Lys Gln His Leu Tyr Leu Lys Arg Pro Ile Glu Cys
W--> 119           115             120             125
       121 TAC TTT GTA AAG GAT GCT GGT CAG AAG GTG ATG AGG ATT GAT CTA ACA      432
       122 Tyr Phe Val Lys Asp Ala Gly Gln Lys Val Met Arg Ile Asp Leu Thr
W--> 123           130             135             140
       125 CCC CAC AAC CCA TTG TTG GCA AGC GAT GTT AGC ACA ACC ATA ATG GGT      480
       126 Pro His Asn Pro Leu Leu Ala Ser Asp Val Ser Thr Thr Ile Met Gly
W--> 127 145              150             155             160
       129 TAT CCT GAG AGA GAA GGT GAA CTC CGT CAA ACT GGA AAG GCA AGG TTA      528
       130 Tyr Pro Glu Arg Glu Gly Glu Leu Arg Gln Thr Gly Lys Ala Arg Leu
W--> 131           165             170             175
       133 GTC GAC CCA TCA GAG TTG CCC GCG CGG AAT GAG GAT ATT GAT GCA GAG      576
       134 Val Asp Pro Ser Glu Leu Pro Ala Arg Asn Glu Asp Ile Asp Ala Glu
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                    Input Set : N:\Crf3\RULE60\09842347.txt
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W--> 135               180               185               190
     137 TTT GAG AGT CTA AAT CGC ATA AGT GGT TTG CGC GAC TAT AAT CCC ATT      624
     138 Phe Glu Ser Leu Asn Arg Ile Ser Gly Leu Arg Asp Tyr Asn Pro Ile
W--> 139          195               200               205
     141 TCA CAA AAT GTT TGC TTG CTA ACA AAT GAG TCA GAA GGC CAT AGA GAG      672
     142 Ser Gln Asn Val Cys Leu Leu Thr Asn Glu Ser Glu Gly His Arg Glu
W--> 143     210               215               220
     145 AAG ATG TTT GGA ATT GGA TAT GGT TCA GTG ATC ATT ACA AAT CAA CAT      720
     146 Lys Met Phe Gly Ile Gly Tyr Gly Ser Val Ile Ile Thr Asn Gln His
W--> 147 225               230               235               240
     149 CTG TTC AGA AGG AAT AAT GGG GAG TTA TCA ATT CAA TCC AAG CAT GGC      768
     150 Leu Phe Arg Arg Asn Asn Gly Glu Leu Ser Ile Gln Ser Lys His Gly
W--> 151               245               250               255
     153 TAC TTC AGA TGC CGC AAC ACC ACA AGC TTG AAG ATG CTG CCT TTG GAG      816
     154 Tyr Phe Arg Cys Arg Asn Thr Thr Ser Leu Lys Met Leu Pro Leu Glu
W--> 155          260               265               270
     157 GGA CAT GAC ATT TTG TTG ATT CAG TTA CCA AGG GAC TTT CCA GTG TTT      864
     158 Gly His Asp Ile Leu Leu Ile Gln Leu Pro Arg Asp Phe Pro Val Phe
W--> 159          275               280               285
     161 CCA CAA AAG ATT CGC TTT AGG GAG CCA AGA GTG GAT GAC AAA ATT GTT      912
     162 Pro Gln Lys Ile Arg Phe Arg Glu Pro Arg Val Asp Asp Lys Ile Val
W--> 163     290               295               300
     165 TTG GTC AGC ACA AAT TTC CAG GAA AAG AGT TCC TCG AGC ACG GTC TCA      960
     166 Leu Val Ser Thr Asn Phe Gln Glu Lys Ser Ser Ser Ser Thr Val Ser
W--> 167 305               310               315               320
     169 GAG TCC AGT AAC ATT TCA AGA GTG CAG TCA GCC AAT TTC TAC AAG CAT     1008
     170 Glu Ser Ser Asn Ile Ser Arg Val Gln Ser Ala Asn Phe Tyr Lys His
W--> 171               325               330               335
     173 TGG ATC TCA ACA GTA GCA GGA CAC TGT GGA AAC CCT ATG GTT TCG ACT     1056
     174 Trp Ile Ser Thr Val Ala Gly His Cys Gly Asn Pro Met Val Ser Thr
W--> 175          340               345               350
     177 AAA GAT GGA TTT ATT GTA GGT ATC CAC AGT CTT GCT TCA TTG ACA GGC     1104
     178 Lys Asp Gly Phe Ile Val Gly Ile His Ser Leu Ala Ser Leu Thr Gly
W--> 179          355               360               365
     181 GAC GTT AAC ATC TTC ACA AGC TTT CCG CCG CAG TTT GAG AAC AAA TAT     1152
     182 Asp Val Asn Ile Phe Thr Ser Phe Pro Pro Gln Phe Glu Asn Lys Tyr
W--> 183     370               375               380
     185 CTA CAG AAG CTC AGT GAA CAC ACA TGG TGT AGT GGA TGG AAA CTA AAT     1200
     186 Leu Gln Lys Leu Ser Glu His Thr Trp Cys Ser Gly Trp Lys Leu Asn
W--> 187 385               390               395               400
     189 CTT GGA AAG ATT AGT TGG GGT GGA ATC AAC ATT GTG GAG GAT GCA CCT     1248
     190 Leu Gly Lys Ile Ser Trp Gly Gly Ile Asn Ile Val Glu Asp Ala Pro
W--> 191               405               410               415
     193 GAA GAG CCC TTT ATA ACA TCC AAG ATG GCA AGC CTT CTT AGT GAT TTG     1296
     194 Glu Glu Pro Phe Ile Thr Ser Lys Met Ala Ser Leu Leu Ser Asp Leu
W--> 195          420               425               430
     197 AAT TGT TCA TTC CAA GCA AGT GCG                                     1320
     198 Asn Cys Ser Phe Gln Ala Ser Ala
W--> 199          435               440
```

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```
202 (2) INFORMATION FOR SEQ ID NO: 2:
204      (i) SEQUENCE CHARACTERISTICS:
205          (A) LENGTH: 440 amino acids
206          (B) TYPE: amino acid
207          (D) TOPOLOGY: linear
209     (ii) MOLECULE TYPE: protein
211     (vi) ORIGINAL SOURCE:
212          (A) ORGANISM: Clover Yellow Vein Virus
214     (ix) FEATURE:
215          (A) NAME/KEY: mat_peptide
216          (B) LOCATION: 4..437
217          (D) OTHER INFORMATION:
220     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
222 Lys Phe Gln Gly Lys Ser Lys Arg Thr Arg Gln Lys Leu Lys Phe Arg
223   1           5               10              15
225 Ala Ala Arg Asp Met Lys Asp Arg Tyr Glu Val His Ala Asp Glu Gly
226             20              25              30
228 Thr Leu Val Glu Asn Phe Gly Thr Arg Tyr Ser Lys Lys Gly Lys Thr
229         35              40              45
231 Lys Gly Thr Val Val Gly Leu Gly Ala Lys Thr Arg Arg Phe Thr Asn
232      50              55              60
234 Met Tyr Gly Phe Asp Pro Thr Glu Tyr Ser Phe Ala Arg Tyr Leu Asp
235  65              70              75              80
237 Pro Ile Thr Gly Ala Thr Leu Asp Glu Thr Pro Ile His Asn Val Asn
238              85              90              95
240 Leu Val Ala Glu His Phe Gly Asp Ile Arg Leu Asp Met Val Asp Lys
241             100             105             110
243 Glu Leu Leu Asp Lys Gln His Leu Tyr Leu Lys Arg Pro Ile Glu Cys
244         115             120             125
246 Tyr Phe Val Lys Asp Ala Gly Gln Lys Val Met Arg Ile Asp Leu Thr
247     130             135             140
249 Pro His Asn Pro Leu Leu Ala Ser Asp Val Ser Thr Thr Ile Met Gly
250 145             150             155             160
252 Tyr Pro Glu Arg Glu Gly Glu Leu Arg Gln Thr Gly Lys Ala Arg Leu
253             165             170             175
255 Val Asp Pro Ser Glu Leu Pro Ala Arg Asn Glu Asp Ile Asp Ala Glu
256         180             185             190
258 Phe Glu Ser Leu Asn Arg Ile Ser Gly Leu Arg Asp Tyr Asn Pro Ile
259         195             200             205
261 Ser Gln Asn Val Cys Leu Leu Thr Asn Glu Ser Glu Gly His Arg Glu
262     210             215             220
264 Lys Met Phe Gly Ile Gly Tyr Gly Ser Val Ile Ile Thr Asn Gln His
265 225             230             235             240
267 Leu Phe Arg Arg Asn Asn Gly Glu Leu Ser Ile Gln Ser Lys His Gly
268             245             250             255
270 Tyr Phe Arg Cys Arg Asn Thr Thr Ser Leu Lys Met Leu Pro Leu Glu
271         260             265             270
273 Gly His Asp Ile Leu Leu Ile Gln Leu Pro Arg Asp Phe Pro Val Phe
274         275             280             285
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276 Pro Gln Lys Ile Arg Phe Arg Glu Pro Arg Val Asp Asp Lys Ile Val
277     290             295             300
279 Leu Val Ser Thr Asn Phe Gln Glu Lys Ser Ser Ser Ser Thr Val Ser
280 305             310             315             320
282 Glu Ser Ser Asn Ile Ser Arg Val Gln Ser Ala Asn Phe Tyr Lys His
283             325             330             335
285 Trp Ile Ser Thr Val Ala Gly His Cys Gly Asn Pro Met Val Ser Thr
286             340             345             350
288 Lys Asp Gly Phe Ile Val Gly Ile His Ser Leu Ala Ser Leu Thr Gly
289         355             360             365
291 Asp Val Asn Ile Phe Thr Ser Phe Pro Pro Gln Phe Glu Asn Lys Tyr
292     370             375             380
294 Leu Gln Lys Leu Ser Glu His Thr Trp Cys Ser Gly Trp Lys Leu Asn
295 385             390             395             400
297 Leu Gly Lys Ile Ser Trp Gly Gly Ile Asn Ile Val Glu Asp Ala Pro
298             405             410             415
300 Glu Glu Pro Phe Ile Thr Ser Lys Met Ala Ser Leu Leu Ser Asp Leu
301             420             425             430
303 Asn Cys Ser Phe Gln Ala Ser Ala
304         435             440
306 (2) INFORMATION FOR SEQ ID NO: 3:
308      (i) SEQUENCE CHARACTERISTICS:
309            (A) LENGTH: 25 base pairs
310            (B) TYPE: nucleic acid
311            (C) STRANDEDNESS: single
312            (D) TOPOLOGY: linear
314      (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
W--> 316     (iii) HYPOTHETICAL: N
W--> 318     (iv) ANTI-SENSE: N
322          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
324 GTCCATGGGG AAAAGTAAGA GAACA                                    25
326 (2) INFORMATION FOR SEQ ID NO: 4:
328      (i) SEQUENCE CHARACTERISTICS:
329            (A) LENGTH: 20 base pairs
330            (B) TYPE: nucleic acid
331            (C) STRANDEDNESS: single
332            (D) TOPOLOGY: linear
334      (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
W--> 336     (iii) HYPOTHETICAL: N
W--> 338     (iv) ANTI-SENSE: N
342          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
344 ACTCTGAGAC CGTGCTCGAG                                          20
346 (2) INFORMATION FOR SEQ ID NO: 5:
348      (i) SEQUENCE CHARACTERISTICS:
349            (A) LENGTH: 20 base pairs
350            (B) TYPE: nucleic acid
351            (C) STRANDEDNESS: single
352            (D) TOPOLOGY: linear
354      (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
```

VERIFICATION SUMMARY   DATE: 05/04/2001
PATENT APPLICATION: US/09/842,347   TIME: 12:40:34

                  Input Set : N:\Crf3\RULE60\09842347.txt
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L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:69 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=1
L:71 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=1
L:115 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:119 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:123 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:127 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:131 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:135 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:139 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:143 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:147 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:151 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:155 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:159 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:163 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:167 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:171 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:175 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:179 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:183 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:187 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:191 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:195 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:199 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:316 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=3
L:318 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=3
L:336 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=4
L:338 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=4
L:356 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=5
L:358 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=5
L:376 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=6
L:378 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=6
L:396 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=7
L:398 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=7
L:416 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=8
L:418 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=8
L:436 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=9
L:455 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=10
L:474 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=11
L:476 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=11
L:769 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=13
L:771 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=13
L:789 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=14
L:791 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=14
L:811 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=15
L:813 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=15

VERIFICATION SUMMARY   DATE: 05/04/2001
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Input Set : **N:\Crf3\RULE60\09842347.txt**
Output Set: **N:\CRF3\05042001\I842347.raw**

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L:831 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=16
L:833 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=16
L:851 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=17
L:853 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=17
L:871 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=18
L:873 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=18
L:894 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
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